```
=================================================================
Sequence Listing could not be accepted due to errors.
See attached Validation Report.
If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).
Reviewer: Anne Corrigan
Timestamp: Wed Aug 08 14:07:27 EDT 2007
=================================================================



*******************************************************************
Reviewer Comments:
 <160>  13

Although the above <160> response is "13," 18 sequences are shown in the
submitted file.  See below:

    <210>  18
    <211>  225
    <212>  PRT
    <213>  Mus musculus


    <400>  18

    Met Leu Leu Thr Leu Ala Gly Gly Ala Leu Phe Phe Pro Gly Leu Phe

(the above is a sample of Sequence 18, the last sequence in the file)


*******************************************************************
```

Application No: 10536772   Version No: 2.0

Input Set:

Output Set:

Started:	2007-08-06 11:18:39.445
Finished:	2007-08-06 11:18:41.545
Elapsed:	0 hr(s) 0 min(s) 2 sec(s) 100 ms
Total Warnings:	11
Total Errors:	13
No. of SeqIDs Defined:	13
Actual SeqID Count:	18

Error code		Error Description
E	201	Mandatory field data missing in <223> in SEQ ID (1)
W	213	Artificial or Unknown found in <213> in SEQ ID (3)
E	224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (3)
W	213	Artificial or Unknown found in <213> in SEQ ID (4)
E	224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (4)
W	213	Artificial or Unknown found in <213> in SEQ ID (5)
E	224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (5)
W	213	Artificial or Unknown found in <213> in SEQ ID (6)
E	224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (6)
W	213	Artificial or Unknown found in <213> in SEQ ID (7)
E	224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (7)
W	213	Artificial or Unknown found in <213> in SEQ ID (8)
E	224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (8)
W	213	Artificial or Unknown found in <213> in SEQ ID (9)
E	224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (9)
W	213	Artificial or Unknown found in <213> in SEQ ID (10)

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              Input Set:


              Output Set:



             Started:   2007-08-06 11:18:39.445
            Finished:   2007-08-06 11:18:41.545
             Elapsed:   0 hr(s) 0 min(s) 2 sec(s) 100 ms
      Total Warnings:   11
        Total Errors:   13
 No. of SeqIDs Defined:   13
   Actual SeqID Count:   18
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Error code	Error Description
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (13)
E 252	Calc# of Seq. differs from actual; 13 seqIds defined; count=18

<110>   SHANGHAI CANCER INSTITUTE

<120>   A HUMAN TUMOR-ASSOCIATED GENE CT120 ON CHROMOSOME 17P 13.3 REGION AND PROTEIN ENCODED BY IT

<130>   024832pc

<140>   10536772
<141>   2005-05-26

<150>
<151>

<150>   CN 02150730.9
<151>   2002-11-27

<160>   13

<170>   PatentIn version 3.1

<210>   1
<211>   2145
<212>   DNA
<213>   Homo sapiens

<220>
<221>   CDS
<222>   (91)..(861)
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gccagcgagg cggccggacc cgcagccccg atg ctg ctg acg ctg gcc ggg ggc   114
                                   Met Leu Leu Thr Leu Ala Gly Gly
                                    1   5

gcg ctc ttc ttc ccg ggg ctc ttc gcg ctc tgc acc tgg gcg ctg cgc   162
Ala Leu Phe Phe Pro Gly Leu Phe Ala Leu Cys Thr Trp Ala Leu Arg
    10   15   20

cac tcc cag ccc gga tgg agc cgc acc gac tgc gtg atg atc agc acc   210
His Ser Gln Pro Gly Trp Ser Arg Thr Asp Cys Val Met Ile Ser Thr
25   30   35   40

agg ctg gtt tcc tcg gtg cac gcc gtg ctg gcc acc ggc tcg ggg atc   258
Arg Leu Val Ser Ser Val His Ala Val Leu Ala Thr Gly Ser Gly Ile
                45   50   55

gtc atc att cgc tcc tgc gac gac gtg atc acc ggc agg cac tgg ctt   306
Val Ile Ile Arg Ser Cys Asp Asp Val Ile Thr Gly Arg His Trp Leu
                60   65   70

gcc cgg gaa tat gtg tgg ttt ctg att cca tac atg atc tat gac tcg   354
Ala Arg Glu Tyr Val Trp Phe Leu Ile Pro Tyr Met Ile Tyr Asp Ser
            75   80   85

tac gcc atg tac ctc tgt gaa tgg tgc cga acc aga gac cag aac cgt   402
Tyr Ala Met Tyr Leu Cys Glu Trp Cys Arg Thr Arg Asp Gln Asn Arg
        90   95   100

gcg ccc tcc ctc act ctt cga aac ttc cta agt cga aac cgc ctc atg   450

```
Ala Pro Ser Leu Thr Leu Arg Asn Phe Leu Ser Arg Asn Arg Leu Met
105                 110                 115                 120
atc aca cat cat gcg gtc att ctc ctt gtc ctt gtg cca gtc gca cag        498
Ile Thr His His Ala Val Ile Leu Leu Val Leu Val Pro Val Ala Gln
                125                 130                 135
agg ctc cgg gga gac ctt ggg gac ttc ttt gtc ggc tgc atc ttc acg        546
Arg Leu Arg Gly Asp Leu Gly Asp Phe Phe Val Gly Cys Ile Phe Thr
                140                 145                 150
gca gaa ctg agc act ccg ttt gtg tcg ctg ggc agg gtt ctg att cag        594
Ala Glu Leu Ser Thr Pro Phe Val Ser Leu Gly Arg Val Leu Ile Gln
                155                 160                 165
cta aag cag cag cac acc ctt ctg tac aag gtg aat gga atc ctc acg        642
Leu Lys Gln Gln His Thr Leu Leu Tyr Lys Val Asn Gly Ile Leu Thr
        170                 175                 180
ctg gcc acc ttc ctt tcc tgc cgg atc ctt ctc ttc ccc ttc atg tac        690
Leu Ala Thr Phe Leu Ser Cys Arg Ile Leu Leu Phe Pro Phe Met Tyr
185                 190                 195                 200
tgg tcc tat ggc cgc cag cag gga cta agc ctg ctc caa gta ccc ttc        738
Trp Ser Tyr Gly Arg Gln Gln Gly Leu Ser Leu Leu Gln Val Pro Phe
                205                 210                 215
agc atc cca ttc tac tgc aac gtg gcc aat gcc ttc ctc gta gct cct        786
Ser Ile Pro Phe Tyr Cys Asn Val Ala Asn Ala Phe Leu Val Ala Pro
                220                 225                 230
cag atc tac tgg ttc tgt ctg ctg tgc agg aag gca gtc cgg ctc ttt        834
Gln Ile Tyr Trp Phe Cys Leu Leu Cys Arg Lys Ala Val Arg Leu Phe
        235                 240                 245
gac act ccc caa gcc aaa aag gat ggc taaatgctcc tgggagtcag            881
Asp Thr Pro Gln Ala Lys Lys Asp Gly
        250                 255
gcgcagcctc acaccagctg cctcctccac tcagcattcc atggaccaaa ttgtgccctg       941
ggtagcctca gactttgggt attgataagc cgatggattt gagttttct aaagaatatt      1001
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tcgtttacta gataacccat tggttctttg cctcatcctc tcatccatgg gtcagagttg      1421
aattcttatg tctatagact tccaatcaga agtctcactg gtggggctgg gggtgggggc      1481
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cagaggctgt tctttttcac acacccctcc atgcccggct ttccccatat ccacatgcag      1661
agggcgagct cataaaacta cagggaagcg tgaaatgatg gctttggtag ctgtttactg      1721
ggtaacccca ctgtgacact gtccttttca tgtgatgtgg aaacctactt ctgtcctcca      1781
aaccatgaaa tgtgtcatct agactgcaga gtactcgagt gctttgcctc ccgatatgcc      1841
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tgcggagtga ggcggcagct agcctggcca gtggctgtcc cgtggaccga cacctgcgcc      1961
cccttctgca agcaggattt tctggtgcca acactcattc atcattcccg atcaactagg      2021
atgaatttaa gactgtgcta ccatgtgttc tcaagtggta gtttaaaaag tggatttta      2081
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aaaa                                                                   2145

<210> 2
<211> 257
<212> PRT
<213> Homo sapiens
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<400> 2

Met Leu Leu Thr Leu Ala Gly Gly Ala Leu Phe Phe Pro Gly Leu Phe
1   5   10   15

Ala Leu Cys Thr Trp Ala Leu Arg His Ser Gln Pro Gly Trp Ser Arg
            20   25   30

Thr Asp Cys Val Met Ile Ser Thr Arg Leu Val Ser Ser Val His Ala
        35   40   45

Val Leu Ala Thr Gly Ser Gly Ile Val Ile Arg Ser Cys Asp Asp
    50   55   60

Val Ile Thr Gly Arg His Trp Leu Ala Arg Glu Tyr Val Trp Phe Leu
65   70   75   80

Ile Pro Tyr Met Ile Tyr Asp Ser Tyr Ala Met Tyr Leu Cys Glu Trp
                85   90   95

Cys Arg Thr Arg Asp Gln Asn Arg Ala Pro Ser Leu Thr Leu Arg Asn
            100   105   110

Phe Leu Ser Arg Asn Arg Leu Met Ile Thr His His Ala Val Ile Leu
        115   120   125

Leu Val Leu Val Pro Val Ala Gln Arg Leu Arg Gly Asp Leu Gly Asp
    130   135   140

Phe Phe Val Gly Cys Ile Phe Thr Ala Glu Leu Ser Thr Pro Phe Val
145   150   155   160

Ser Leu Gly Arg Val Leu Ile Gln Leu Lys Gln Gln His Thr Leu Leu
            165   170   175

Tyr Lys Val Asn Gly Ile Leu Thr Leu Ala Thr Phe Leu Ser Cys Arg
            180   185   190

Ile Leu Leu Phe Pro Phe Met Tyr Trp Ser Tyr Gly Arg Gln Gln Gly
        195   200   205

Leu Ser Leu Leu Gln Val Pro Phe Ser Ile Pro Phe Tyr Cys Asn Val
    210   215   220

Ala Asn Ala Phe Leu Val Ala Pro Gln Ile Tyr Trp Phe Cys Leu Leu
225   230   235   240

Cys Arg Lys Ala Val Arg Leu Phe Asp Thr Pro Gln Ala Lys Lys Asp
            245   250   255

Gly

<210> 3
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<213> Artificial

<220>
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<223> primer

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<210> 4
<211> 23
<212> DNA
<213> Artificial

<220>
<221> misc_feature
<222> (1)..(23)

<223> primer

<400> 4
cgaatgatga cgatccccga gcc   23

<210> 5
<211> 22
<212> DNA
<213> Artificial

<220>
<221> misc_feature
<222> (1)..(22)
<223> primer

<400> 5
ccgatgctgc tgacgctggc cg   22

<210> 6
<211> 25
<212> DNA
<213> Artificial

<220>
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<222> (1)..(25)
<223> primer

<400> 6
tgttggcacc agaaaatcct gcttg   25

<210> 7
<211> 20
<212> DNA
<213> Artificial

<220>
<221> misc_feature
<222> (1)..(20)
<223> primer

<400> 7
aagtactccg tgtggatcgg   20

<210> 8
<211> 20
<212> DNA
<213> Artificial

<220>
<221> misc_feature
<222> (1)..(20)
<223> primer

<400> 8
tcaagttggg ggacaaaaag   20

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<210>   9
<211>   25
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<213>   Artificial

<220>
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<222>   (1)..(25)
<223>   primer

<400>   9
gtgcgactgg cacaaggaca aagag                                              25


<210>   10
<211>   23
<212>   DNA
<213>   Artificial

<220>
<221>   misc_feature
<222>   (1)..(23)
<223>   primer

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ggggatcgtc atcattcgct cct                                               23


<210>   11
<211>   15
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<213>   Artificial

<220>
<221>   MISC_FEATURE
<222>   (1)..(15)
<223>   oligopeptide corresponding to C-terminus of CT120 protein

<400>   11

Cys Arg Lys Ala Val Arg Leu Phe Asp Thr Pro Gln Ala Lys Lys
1               5                   10                  15


<210>   12
<211>   20
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<213>   Artificial

<220>
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<222>   (1)..(20)
<223>   primer

<400>   12
atgctgctga cgctggccgg                                                   20


<210>   13
<211>   20
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<213> Artificial

<220>
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<222> (1)..(20)
<223> primer

<400> 13
ttagccatcc tttttggctt   20

<210> 14
<211> 224
<212> PRT
<213> Homo sapiens

<400> 14

Met Ala Ser Thr Ala Gly Tyr Ile Val Ser Thr Ser Cys Lys His Ile
1   5   10   15
Ile Asp Asp Gln His Trp Leu Ser Ser Ala Tyr Thr Gln Phe Ala Val
            20   25   30
Pro Tyr Phe Ile Tyr Asp Ile Tyr Ala Met Phe Leu Cys His Trp His
            35   40   45
Lys His Gln Val Lys Gly His Gly Gly Asp Asp Gly Ala Ala Arg Ala
        50   55   60
Pro Gly Ser Thr Trp Ala Ile Ala Arg Gly Tyr Leu His Lys Glu Phe
65   70   75   80
Leu Met Val Leu His His Ala Ala Met Val Leu Val Cys Phe Pro Leu
                85   90   95
Ser Val Val Trp Arg Gln Gly Lys Gly Asp Phe Phe Leu Gly Cys Met
                100   105   110
Leu Met Ala Glu Val Ser Thr Pro Phe Val Cys Leu Gly Lys Ile Leu
            115   120   125
Ile Gln Tyr Lys Gln Gln His Thr Leu Leu His Lys Val Asn Gly Ala
        130   135   140
Leu Met Leu Leu Ser Phe Leu Cys Cys Arg Val Leu Leu Phe Pro Tyr
145   150   155   160
Leu Tyr Trp Ala Tyr Gly Arg His Ala Gly Leu Pro Leu Leu Ala Val
                165   170   175
Pro Leu Ala Ile Pro Ala His Val Asn Leu Gly Ala Ala Leu Leu Leu
            180   185   190
Ala Pro Gln Leu Tyr Trp Phe Phe Leu Ile Cys Arg Gly Ala Cys Arg
            195   200   205
Leu Phe Trp Pro Arg Ser Arg Pro Pro Pro Ala Cys Gln Ala Gln Asp
    210   215   220

<210> 15
<211> 275
<212> PRT
<213> Homo sapiens

<400> 15

Met Leu Thr Pro Met Val Ala Gly Gly Val Val Phe Pro Gly Leu Phe
1   5   10   15
Leu Leu Ser Lys Asn Thr Leu Gln Arg Leu Pro Gln Leu Arg Trp Glu

Glu Ala Asp Ala Val Ile Val Ser Ala Arg Leu Val Ser Ser Val Gln
                    35   40   45
Ala Ile Met Ala Ser Thr Ala Gly Tyr Ile Val Ser Thr Ser Cys Lys
          50   55   60
His Ile Ile Asp Asp Gln His Trp Leu Ser Ser Ala Tyr Thr Gln Phe
65   70   75   80
Ala Val Pro Tyr Phe Ile Tyr Asp Ile Tyr Ala Met Phe Leu Cys His
                    85   90   95
Trp His Lys His Gln Val Lys Gly His Gly Gly Glu Asp Gly Thr Pro
                    100   105   110
Arg Ala Leu Gly Ser Thr Trp Ala Val Val Arg Gly Tyr Leu His Lys
          115   120   125
Glu Phe Leu Met Val Leu His His Ala Ala Met Val Leu Val Cys Phe
          130   135   140
Pro Leu Ser Val Val Trp Arg Gln Gly Lys Gly Asp Phe Phe Leu Gly
145   150   155   160
Cys Met Leu Met Ala Glu Val Ser Thr Pro Phe Val Cys Leu Gly Lys
                    165   170   175
Ile Leu Ile Gln Tyr Lys Gln Gln His Thr Leu Leu His Lys Val Asn
                    180   185   190
Gly Ala Leu Met Leu Leu Ser Phe Leu Cys Cys Arg Val Leu Leu Phe
          195   200   205
Pro Tyr Leu Tyr Trp Ala Tyr Gly Arg His Ala Gly Leu Pro Leu Leu
          210   215   220
Ser Val Pro Met Ala Ile Pro Ala His Val Asn Leu Gly Ala Ala Leu
225   230   235   240
Leu Leu Ala Pro Gln Leu Tyr Trp Phe Phe Leu Ile Cys Arg Gly Ala
                    245   250   255
Cys Arg Leu Phe Arg Pro Arg Gly Ser Pro Pro Pro Ser Pro Cys Gln
                    260   265   270
Thr Gln Asp
          275

Leu Ala Ile Pro Ser Ser Pro Pro Thr Pro Ser Leu Asn Leu Ala Phe
1   5   10   15
Leu Ser Leu Leu Asp Pro Leu Val Ser Leu Pro Gly Phe Lys Ser Pro
                    20   25   30
Cys Leu Pro Gln Trp Trp Leu Gly Gly Trp Cys Ser Pro Asp Ser Ser
          35   40   45
Ser Tyr Pro Arg Thr Arg Ser Arg Gly Cys Pro Ser Cys Ala Gly Arg
          50   55   60
Glu Ala Asp Ala Val Ile Val Ser Ala Arg Leu Val Ser Ser Val Gln
65   70   75   80
Ala Ile Met Ala Ser Thr Ala Gly Tyr Ile Val Ser Thr Ser Cys Lys
                    85   90   95
His Ile Ile Asp Asp Gln His Trp Leu Ser Ser Ala Tyr Thr Gln Phe
                    100   105   110
Ala Val Pro Tyr Phe Ile Tyr Asp Ile Tyr Ala Met Phe Leu Cys His
          115   120   125

```
Trp His Lys His Gln Val Lys Gly His Gly Gly Glu Asp Gly Thr Pro
    130                 135                 140
Arg Ala Leu Gly Ser Thr Trp Ala Val Val Arg Gly Tyr Leu His Lys
145                 150                 155                 160
Glu Phe Leu Met Val Leu His His Ala Ala Met Val Leu Val Cys Phe
                165                 170                 175
Pro Leu Ser Val Val Trp Arg Gln Gly Lys Gly Asp Phe Phe Leu Gly
                180                 185                 190
Cys Met Leu Met Ala Glu Val Ser Thr Pro Phe Val Cys Leu Gly Lys
            195                 200                 205
Ile Leu Ile Gln Tyr Lys Gln Gln His Thr Leu Leu His Lys Val
```